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Pat 09/719,748

RAW SEQUENCE LISTING DATE: 06/12/2001
PATENT APPLICATION: US/09/719,748 TIME: 11:47:46

Input Set : A:\KIMCHI2A.txt
Output Set: N:\CRF3\06122001\I719748.raw


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 3 <110> APPLICANT: KIMCHI, Adi
 5 <120> TITLE OF INVENTION: DAP-KINASE RELATED PROTEIN
 7 <130> FILE REFERENCE: KIMCHI2A
 9 <140> CURRENT APPLICATION NUMBER: 09/719,748
10 <141> CURRENT FILING DATE: 2000-12-15
12 <150> PRIOR APPLICATION NUMBER: 60/089,294
13 <151> PRIOR FILING DATE: 1998-06-15
15 <160> NUMBER OF SEQ ID NOS: 14
17 <170> SOFTWARE: PatentIn Ver. 2.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1742
21 <212> TYPE: DNA
22 <213> ORGANISM: Human
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (62)..(1141)
28 <400> SEQUENCE: 1
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31 c atg gag cca ttc aag cag cag aag gtg gag gac ttt tat gac atc gga 109
32   Met Glu Pro Phe Lys Gln Gln Lys Val Glu Asp Phe Tyr Asp Ile Gly
33     1               5                  10                  15
35 gag gag ctg ggg agt ggc cag ttt gcc atc gtg aag aag tgc cgg gag   157
36 Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Lys Lys Cys Arg Glu
37             20                  25                  30
39 aag agc acg ggg ctt gag tat gca gcc aag ttc atc aag aag cgg cag   205
40 Lys Ser Thr Gly Leu Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg Gln
41          35                  40                  45
43 agc cgg gcg agc cgg cgc ggt gtg agc cgg gag gag atc gag cgg gag   253
44 Ser Arg Ala Ser Arg Arg Gly Val Ser Arg Glu Glu Ile Glu Arg Glu
45      50                  55                  60
47 gtg agc atc ctg cgg cag gtg ctg cac cac aat gtc atc acg ctg cac   301
48 Val Ser Ile Leu Arg Gln Val Leu His His Asn Val Ile Thr Leu His
49  65                  70                  75                  80
51 gac gtc tat gag aac cgc acc gac gtg gtg cac atc ctt gag cta gtg   349
52 Asp Val Tyr Glu Asn Arg Thr Asp Val Val His Ile Leu Glu Leu Val
53                  85                  90                  95
55 tct gga gga gag ctc ttc gat ttc ctg gcc cag aag gag tca ctg agt   397
56 Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Gln Lys Glu Ser Leu Ser
57             100                 105                 110
59 gag gag gag gcc acc agc ttc att aag cag atc ctg gat ggg gtg aac   445
60 Glu Glu Glu Ala Thr Ser Phe Ile Lys Gln Ile Leu Asp Gly Val Asn
61         115                 120                 125
63 tac ctt cac aca aag aaa att gct cac ttt gat ctc aag cca gaa aac   493
64 Tyr Leu His Thr Lys Lys Ile Ala His Phe Asp Leu Lys Pro Glu Asn
65     130                 135                 140
67 att atg ttg tta gac aag aat att ccc att cca cac atc aag ctg att   541
68 Ile Met Leu Leu Asp Lys Asn Ile Pro Ile Pro His Ile Lys Leu Ile
```

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69 145                 150                 155                 160
71 gac ttt ggt ctg gct cac gaa ata gaa gat gga gtt gaa ttt aag aat   589
72 Asp Phe Gly Leu Ala His Glu Ile Glu Asp Gly Val Glu Phe Lys Asn
73                  165                 170                 175
75 att ttt ggg acg ccg gaa ttt gtt gct cca gaa att gtg aac tac gag   637
76 Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr Glu
77              180                 185                 190
79 ccc ctg ggt ctg gag gct gac atg tgg agc ata ggc gtc atc acc tac   685
80 Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr Tyr
81          195                 200                 205
83 atc ctc tta agt gga gca tcc cct ttc ctg gga gac acg aag cag gaa   733
84 Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln Glu
85      210                 215                 220
87 aca ctg gca aat atc aca tca gtg agt tac gac ttt gat gag gaa ttc   781
88 Thr Leu Ala Asn Ile Thr Ser Val Ser Tyr Asp Phe Asp Glu Glu Phe
89 225                 230                 235                 240
91 ttc agc cat acg agc gag ctg gcc aag gac ttt att cgg aag ctt ctg   829
92 Phe Ser His Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu Leu
93                  245                 250                 255
95 gtt aaa gag acc cgg aaa cgg ctc aca atc caa gag gct ctc aga cac   877
96 Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg His
97              260                 265                 270
99 ccc tgg atc acg ccg gtg gac aac cag caa gcc atg gtg cga cgg gag   925
100 Pro Trp Ile Thr Pro Val Asp Asn Gln Gln Ala Met Val Arg Arg Glu
101         275                 280                 285
103 tct gtg gtc aat ctg gag aac ttc agg aag cag tat gtc cgc agg cgg   973
104 Ser Val Val Asn Leu Glu Asn Phe Arg Lys Gln Tyr Val Arg Arg Arg
105     290                 295                 300
107 tgg aag ctt tcc ttc agc atc gtg tcc ctg tgc aac cac ctc acc cgc   1021
108 Trp Lys Leu Ser Phe Ser Ile Val Ser Leu Cys Asn His Leu Thr Arg
109 305                 310                 315                 320
111 tcg ctg atg aag aag gtg cac ctg agg ccg gat gag gac ctg agg aac   1069
112 Ser Leu Met Lys Lys Val His Leu Arg Pro Asp Glu Asp Leu Arg Asn
113                 325                 330                 335
117 tgt gag agt gac act gag gag gac atc gcc agg agg aaa gcc ctc cac   1117
118 Cys Glu Ser Asp Thr Glu Glu Asp Ile Ala Arg Arg Lys Ala Leu His
119             340                 345                 350
121 cca cgg agg agg agc agc acc tcc taactggcct gacctgcagt ggccgccagg  1171
122 Pro Arg Arg Arg Ser Ser Thr Ser
123         355                 360
125 gaggtttggg cccagcgggg ctcccttctg tgcagacttt tggacccagc tcagcaccag 1231
127 cacccgggcg tcctgagcac tttgcaagag agatgggccc aaggaattca gaagagcttg 1291
129 caggcaagcc aggagaccct gggagctgtg gctgtcttct gtggaggagg ctccagcatt 1351
131 cccaaagctc ttaattctcc ataaaatggg ctttcctctg tctgccatcc tcagagtctg 1411
133 gggtgggagt gtggacttag gaaaacaata taaaggacat cctcatcatc acggggtgaa 1471
135 ggtcagagta aggcagcctt cttcacaggc tgagggggtt cagaaccagc ctggccaaaa 1531
137 attacaccag agagacagag tcctccccat tgggaacagg gtgattgagg aaagtgaacc 1591
139 ttgggtgtga gggaccaatc ctgtgacctc ccagaaccat ggaagccagg acgtcaggct 1651
141 gaccaacacc tcagaccttc tgaagcagcc cattgctggc ccgccatgtt gtaattttgc 1711
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Input Set : A:\KIMCHI2A.txt
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tcatttttat taaacttctg gtttacctga a 1742

<210> SEQ ID NO: 2
<211> LENGTH: 360
<212> TYPE: PRT
<213> ORGANISM: Human
<400> SEQUENCE: 2

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Met Glu Pro Phe Lys Gln Gln Lys Val Glu Asp Phe Tyr Asp Ile Gly
  1               5                  10                  15
Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Lys Lys Cys Arg Glu
             20                  25                  30
Lys Ser Thr Gly Leu Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg Gln
         35                  40                  45
Ser Arg Ala Ser Arg Arg Gly Val Ser Arg Glu Glu Ile Glu Arg Glu
     50                  55                  60
Val Ser Ile Leu Arg Gln Val Leu His His Asn Val Ile Thr Leu His
 65                  70                  75                  80
Asp Val Tyr Glu Asn Arg Thr Asp Val Val His Ile Leu Glu Leu Val
                 85                  90                  95
Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Gln Lys Glu Ser Leu Ser
            100                 105                 110
Glu Glu Glu Ala Thr Ser Phe Ile Lys Gln Ile Leu Asp Gly Val Asn
        115                 120                 125
Tyr Leu His Thr Lys Lys Ile Ala His Phe Asp Leu Lys Pro Glu Asn
    130                 135                 140
Ile Met Leu Leu Asp Lys Asn Ile Pro Ile Pro His Ile Lys Leu Ile
145                 150                 155                 160
Asp Phe Gly Leu Ala His Glu Ile Glu Asp Gly Val Glu Phe Lys Asn
                165                 170                 175
Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr Glu
            180                 185                 190
Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr Tyr
        195                 200                 205
Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln Glu
    210                 215                 220
Thr Leu Ala Asn Ile Thr Ser Val Ser Tyr Asp Phe Asp Glu Glu Phe
225                 230                 235                 240
Phe Ser His Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu Leu
                245                 250                 255
Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg His
            260                 265                 270
Pro Trp Ile Thr Pro Val Asp Asn Gln Gln Ala Met Val Arg Arg Glu
        275                 280                 285
Ser Val Val Asn Leu Glu Asn Phe Arg Lys Gln Tyr Val Arg Arg Arg
    290                 295                 300
Trp Lys Leu Ser Phe Ser Ile Val Ser Leu Cys Asn His Leu Thr Arg
305                 310                 315                 320
Ser Leu Met Lys Lys Val His Leu Arg Pro Asp Glu Asp Leu Arg Asn
                325                 330                 335
Cys Glu Ser Asp Thr Glu Glu Asp Ile Ala Arg Arg Lys Ala Leu His
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Input Set : A:\KIMCHI2A.txt
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216             340                 345                 350
218 Pro Arg Arg Arg Ser Ser Thr Ser
219         355                 360
222 <210> SEQ ID NO: 3
223 <211> LENGTH: 263
224 <212> TYPE: PRT
225 <213> ORGANISM: Human
227 <400> SEQUENCE: 3
228 Tyr Asp Thr Gly Glu Glu Leu Gly Ser Gly Gln Phe Ala Val Val Lys
229  1               5                  10                  15
231 Lys Cys Arg Glu Lys Ser Thr Gly Leu Gln Tyr Ala Ala Lys Phe Ile
232             20                  25                  30
234 Lys Lys Arg Arg Thr Lys Ser Ser Arg Arg Gly Val Ser Arg Glu Asp
235         35                  40                  45
237 Ile Glu Arg Glu Val Ser Ile Leu Lys Glu Ile Gln His Pro Asn Val
238     50                  55                  60
240 Ile Thr Leu His Glu Val Tyr Glu Asn Lys Thr Asp Val Ile Leu Ile
241 65                  70                  75                  80
243 Leu Glu Leu Val Ala Gly Gly Glu Leu Phe Asp Phe Leu Ala Glu Lys
244                 85                  90                  95
246 Glu Ser Leu Thr Glu Glu Glu Ala Thr Glu Phe Leu Lys Gln Ile Leu
247             100                 105                 110
249 Asn Gly Val Tyr Tyr Leu His Ser Leu Gln Ile Ala His Phe Asp Leu
250         115                 120                 125
252 Lys Pro Glu Asn Ile Met Leu Leu Asp Arg Asn Val Pro Lys Pro Arg
253     130                 135                 140
255 Ile Lys Ile Ile Asp Phe Gly Leu Ala His Lys Ile Asp Phe Gly Asn
256 145                 150                 155                 160
258 Glu Phe Lys Asn Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile
259                 165                 170                 175
261 Val Asn Tyr Glu Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly
262             180                 185                 190
264 Val Ile Thr Tyr Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp
265         195                 200                 205
267 Thr Lys Gln Glu Thr Leu Ala Asn Val Ser Ala Val Asn Tyr Glu Phe
268     210                 215                 220
270 Glu Asp Glu Tyr Phe Ser Asn Thr Ser Ala Leu Ala Lys Asp Phe Ile
271 225                 230                 235                 240
273 Arg Arg Leu Leu Val Lys Asp Pro Lys Lys Arg Met Thr Ile Gln Asp
274                 245                 250                 255
276 Ser Leu Gln His Pro Trp Ile
277             260
280 <210> SEQ ID NO: 4
281 <211> LENGTH: 263
282 <212> TYPE: PRT
283 <213> ORGANISM: Human
285 <400> SEQUENCE: 4
286 Tyr Glu Met Gly Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Arg
287  1               5                  10                  15
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```
289 Lys Cys Arg Gln Lys Gly Thr Gly Lys Glu Tyr Ala Ala Lys Phe Ile
290              20                  25                  30
292 Lys Lys Arg Arg Leu Ser Ser Ser Arg Arg Gly Val Ser Arg Glu Glu
293          35                  40                  45
295 Ile Glu Arg Glu Val Asn Ile Leu Arg Glu Ile Arg His Pro Asn Ile
296      50                  55                  60
298 Ile Thr Leu His Asp Ile Phe Glu Asn Lys Thr Asp Val Val Leu Ile
299  65                  70                  75                  80
301 Leu Glu Leu Val Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Glu Lys
302                  85                  90                  95
304 Glu Ser Leu Thr Glu Asp Glu Ala Thr Gln Phe Leu Lys Gln Ile Leu
305             100                 105                 110
307 Asp Gly Val His Tyr Leu His Ser Lys Arg Ile Ala His Phe Asp Leu
308         115                 120                 125
310 Lys Pro Glu Asn Ile Met Leu Leu Asp Lys Asn Val Pro Asn Pro Arg
311     130                 135                 140
313 Ile Lys Leu Ile Asp Phe Gly Ile Ala His Lys Ile Glu Ala Gly Asn
314 145                 150                 155                 160
316 Glu Phe Lys Asn Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile
317                 165                 170                 175
319 Val Asn Tyr Glu Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly
320             180                 185                 190
322 Val Ile Thr Tyr Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Glu
323         195                 200                 205
325 Thr Lys Gln Glu Thr Leu Thr Asn Ile Ser Ala Val Asn Tyr Asp Phe
326     210                 215                 220
328 Asp Glu Glu Tyr Phe Ser Asn Thr Ser Glu Leu Ala Lys Asp Phe Ile
329 225                 230                 235                 240
331 Arg Arg Leu Leu Val Lys Asp Pro Lys Arg Arg Met Thr Ile Ala Gln
332                 245                 250                 255
334 Ser Leu Glu His Ser Trp Ile
335             260
338 <210> SEQ ID NO: 5
339 <211> LENGTH: 261
340 <212> TYPE: PRT
341 <213> ORGANISM: Human
343 <400> SEQUENCE: 5
344 Leu Cys Pro Gly Arg Glu Leu Gly Arg Gly Lys Phe Ala Val Val Arg
345   1               5                  10                  15
347 Lys Cys Ile Lys Lys Asp Ser Gly Lys Glu Phe Ala Ala Lys Phe Met
348              20                  25                  30
350 Arg Lys Arg Arg Lys Gly Gln Asp Cys Arg Met Glu Ile Ile His Glu
351          35                  40                  45
353 Ile Ala Val Leu Glu Leu Ala Gln Asp Asn Pro Trp Val Ile Asn Leu
354      50                  55                  60
356 His Glu Val Tyr Glu Thr Ala Ser Glu Met Ile Leu Val Leu Glu Tyr
357  65                  70                  75                  80
359 Ala Ala Gly Gly Glu Ile Phe Asp Gln Cys Val Ala Asp Arg Glu Glu
360                  85                  90                  95
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VERIFICATION SUMMARY DATE: 06/12/2001
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Input Set : A:\KIMCHI2A.txt
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